SEQUENCE LISTINGS

(1) General Information

    (iii) NUMBER OF SEQUENCES: 4

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS
        (A) LENGTH: 593 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: Linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Leu Glu Arg Leu Lys Ile Tyr Glu Glu Ala Trp Thr Lys Tyr Pro
1               5               10              15

Arg Gly Leu Val Pro Arg Lys Leu Pro Leu Asn Phe Leu Ser Gly Glu
            20              25              30

Lys Phe Lys Glu Cys Leu Asp Arg Phe Leu Arg Met Asn Phe Ser Lys
        35              40              45

Gly Cys Pro Pro Val Phe Asn Thr Leu Arg Ser Leu Tyr Arg Asp Lys
    50              55              60

Glu Lys Val Ala Ile Val Glu Glu Leu Val Val Gly Tyr Glu Thr Ser
65              70              75              80

Leu Lys Ser Cys Arg Leu Phe Asn Pro Asn Asp Asp Gly Lys Glu Glu
            85              90              95

Pro Pro Thr Thr Leu Leu Trp Val Gln Tyr Tyr Leu Ala Gln His Tyr
            100             105             110

Asp Lys Ile Gly Gln Pro Ser Ile Ala Leu Glu Tyr Ile Asn Thr Ala
        115             120             125

Ile Glu Ser Thr Pro Thr Leu Ile Glu Leu Phe Leu Val Lys Ala Lys
    130             135             140

Ile Tyr Lys His Ala Gly Asn Ile Lys Glu Ala Ala Arg Trp Met Asp
145             150             155             160

Glu Ala Gln Ala Leu Asp Thr Ala Asp Arg Phe Ile Asn Ser Lys Cys
            165             170             175

Ala Lys Tyr Met Leu Lys Ala Asn Leu Ile Lys Glu Ala Glu Glu Met
            180             185             190

Cys Ser Lys Phe Thr Arg Glu Gly Thr Ser Ala Val Glu Asn Leu Asn
        195             200             205
```

34

Glu Met Gln Cys Met Trp Phe Gln Thr Glu Cys Ala Gln Ala Tyr Lys
   210   215   220

Ala Met Asn Lys Phe Gly Glu Ala Leu Lys Lys Cys His Glu Ile Glu
225   230   235   240

Arg His Phe Ile Glu Ile Thr Asp Asp Gln Phe Asp Phe His Thr Tyr
          245   250   255

Cys Met Arg Lys Ile Thr Leu Arg Ser Tyr Val Asp Leu Leu Lys Leu
       260   265   270

Glu Asp Val Leu Arg Gln His Pro Phe Tyr Phe Lys Ala Ala Arg Ile
       275   280   285

Ala Ile Glu Ile Tyr Leu Lys Leu His Asp Asn Pro Leu Thr Asp Glu
   290   295   300

Asn Lys Glu His Glu Ala Asp Thr Ala Asn Met Ser Asp Lys Glu Leu
305   310   315   320

Lys Lys Leu Arg Asn Lys Gln Arg Arg Ala Gln Lys Lys Ala Gln Ile
         325   330   335

Glu Glu Glu Lys Lys Asn Ala Glu Lys Glu Lys Pro Gln Arg Asn Pro
       340   345   350

Lys Lys Lys Lys Asp Asp Asp Asp Glu Glu Ile Gly Gly Pro Lys Glu
       355   360   365

Glu Leu Ile Pro Glu Lys Leu Ala Lys Val Glu Thr Pro Leu Glu Glu
   370   375   380

Ala Ile Lys Phe Leu Thr Pro Leu Lys Asn Leu Val Lys Asn Lys Ile
385   390   395   400

Glu Thr His Leu Phe Ala Phe Glu Ile Tyr Phe Arg Lys Glu Lys Phe
         405   410   415

Leu Leu Met Leu Gln Ser Val Lys Arg Ala Phe Ala Ile Asp Ser Ser
       420   425   430

His Pro Trp Leu His Glu Cys Met Ile Arg Leu Phe His Ser Val Cys
       435   440   445

Glu Ser Lys Asp Leu Pro Glu Thr Val Arg Thr Val Leu Lys Gln Glu
   450   455   460

Met Asn Arg Leu Phe Gly Ala Thr Asn Pro Lys Asn Phe Asn Glu Thr
465   470   475   480

Phe Leu Lys Arg Asn Ser Asp Ser Leu Pro His Arg Leu Ser Ala Ala
         485   490   495

Lys Met Val Tyr Tyr Leu Asp Ser Ser Ser Gln Lys Arg Ala Ile Glu
       500   505   510

Leu Ala Thr Thr Leu Asp Gly Ser Leu Thr Asn Arg Asn Leu Gln Thr

Cys Met Glu Val Leu Glu Ala Leu Cys Asp Gly Ser Leu Arg Asp Cys
    530   535   540

Lys Glu Ala Ala Glu Ala Tyr Arg Ala Ser Cys His Lys Leu Phe Pro
545   550   555   560

Tyr Ala Leu Ala Phe Met Pro Pro Gly Tyr Glu Glu Asp Met Lys Ile
                565   570   575

Thr Val Asn Gly Asp Ser Ser Ala Glu Thr Glu Glu Leu Ala Asn Glu
                580   585   590

Ile

(2) INFORMATION FOR SEQ ID NO: 2:

      (i)   SEQUENCE CHARACTERISTICS
          (A) LENGTH: 3418 base pairs
          (B) TYPE: cDNA
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:


```
CAAGTAACAC CCGCAAGATG ATAGAGGATC TGCAGAGTGA GCATCATGGA TTGGTTATGC      60

TTTACCATTT ATTAGAAGAC TATGAAATGG CAGCAAAAAT TTTAGAAGAG TTTAGGAAAA     120

CACAGCAGAC ATCTCCTGAT AAAGTGGATT ATGAATATAG TGAACTCCTC TTATATCAGA     180

ATCAAGTTCT TCGGGAAGCA GGTCTTTATA GAGAAGCCCT GGAACATCTT TGTACCTATG     240

AAAAGCAGAT TTGTGATAAA CTTGCTGTTG AAGAAACCAA AGGGGAACTT CTGTTGCAGT     300

TGTGTCGTTT GGAAGATGCT GCTGACGTTT ATAGAGGATT ACAAGAGAGG AATCCTGAAA     360

ATTGGGCCTA TTACAAAGGC TTAGAAAAAG CACTGAAGCC AGCTAATATG TTAGAACGGC     420

TAAAAATATA TGAGGAAGCC TGGACTAAAT ACCCCAGGGG ACTCGTGCCA AGAAAGCTGC     480

CCTTAAACTT TTTATCTGGA GAGAAGTTTA AGGAGTGTTT GGATAGGTTC CTAAGGATGA     540

ATTTCAGCAA GGGCTGTCCA CCTGTCTTCA ATACCTTGAG GTCTTTATAC AGAGATAAAG     600

AGAAGGTGGC AATCGTAGAA GAACTAGTAG TTGGTTATGA AACTTCTCTA AAAAGTTGTC     660

GCCTATTTAA CCCCAATGAT GATGGAAAGG AGGAACCTCC AACCACATTA CTTTGGGTCC     720

AGTACTATTT GGCACAGCAT TATGATAAAA TTGGTCAGCC ATCCATTGCT CTGGAATACA     780

TAAATACTGC AATTGAAAGT ACACCAACAT TGATAGAACT CTTTCTTGTA AAAGCTAAAA     840
```

```
TCTATAAGCA TGCTGGGAAT ATTAAAGAAG CTGCCAGGTG GATGGATGAA GCCCAGGCCC      900

TGGACACAGC AGACAGATTT ATTAATTCCA AGTGTGCAAA ATACATGTTA AAAGCCAACC      960

TGATTAAAGA GGCTGAAGAA ATGTGTTCCA AGTTTACGAG GGAAGGAACT TCAGCGGTAG     1020

AGAACCTGAA TGAAATGCAG TGTATGTGGT TCCAGACAGA GTGTGCTCAG GCATACAAAG     1080

CAATGAACAA ATTTGGTGAA GCACTTAAGA AATGTCATGA AATTGAGAGA CATTTTATAG     1140

AAATCACCGA TGACCAGTTT GACTTTCATA CATACTGTAT GAGGAAGATC ACCCTTAGAT     1200

CATATGTGGA CTTATTAAAA CTAGAAGATG TACTTCGACA GCATCCATTT TACTTCAAAG     1260

CAGCGAGAAT TGCTATTGAG ATCTATTTGA AGCTTCATGA CAACCCTCTG ACAGATGAGA     1320

ACAAAGAACA CGAGGCTGAT ACAGCAAACA TGTCTGACAA AGAGCTAAAG AAACTGCGTA     1380

ATAAACAAAG AAGAGCTCAA AAGAAAGCCC AGATTGAAGA AGAGAAAAAA AATGCCGAAA     1440

AAGAAAAGCC GCAACGGAAT CCGAAAAAGA AAAAGGATGA TGATGACGAA GAAATTGGAG     1500

GCCCCAAAGA AGAGCTTATC CCTGAGAAAC TGGCCAAGGT TGAAACTCCA TTGGAAGAAG     1560

CTATTAAGTT TTTAACACCA TTGAAGAACT TGGTGAAGAA CAAGATAGAA ACTCATCTTT     1620

TTGCCTTTGA GATCTACTTT AGGAAAGAAA AGTTTCTTTT GATGCTACAA TCAGTAAAGC     1680

GGGCATTTGC TATTGATTCT AGTCATCCCT GGCTTCATGA GTGCATGATT CGACTCTTTC     1740

ATTCTGTGTG TGAAAGTAAA GACTTACCCG AAACAGTTAG AACAGTATTA AAACAAGAAA     1800

TGAATCGTCT TTTTGGAGCA ACAAATCCAA AGAATTTTAA TGAAACCTTT CTGAAAAGGA     1860

ATTCTGATTC ATTGCCACAT AGATTATCAG CTGCCAAAAT GGTATATATT TTAGATTCTT     1920

CTAGTCAAAA ACGAGCAATA GAGCTGGCGA CAACACTTGA TGGATCCCTC ACCAACAGAA     1980

ACCTTCAGAC TTGCATGGAA GTGTTGGAAG CCTTGTGTGA TGGTAGCCTA CGAGACTGTA     2040

AAGAAGCTGC CGAAGCCTAC AGAGCAAGTT GTCATAAGCT TTTCCCTTAT GCTTTGGCTT     2100

TCATGCCTCC TGGATACGAA GAGGATATGA AGATCACAGT GAACGGAGAT AGTTCTGCAG     2160

AAACGGAAGA ACTGGCCAAT GAAATCTGAA CATCATTAAA CAAGCAAATG GAATGACTTT     2220

GGACCATATC TAGTGTATAA TATTTTTGTC ACGCACCTGC TGCATTGCTC TTACTTACAC     2280

AGAATGAGAG GAGTAAATGT TCTTGCCTTC AAATAGTCTT ACGTTTTTTA TCCTGCTGAA     2340

AACTATATAT AAAATATCTA ACATTACAGG ATATAGGTTC AGTTTCTTAA AAAATTAAAA     2400

GCTGCTAAAA TTGAGGGGTT TAAAAGAAAA AAAAATCCGT ATCCTATTCC TACCTTCCCT     2460

TCCCATGTTT TTAACTAATT TATATAAAAT CTGGAGGCTA TAACAGCTAA CATAGCAGGT     2520

GTGTGGCAGA AATATTACTT TAAATTTGTC TTGTGAGATT TTGCTATATC TCAGACAGCA     2580

TAAATAAATG CTGTTTTAGC ACTGGATTCT TTCACTGAGC ACAAAGAGTT GTTGGGGCTT     2640

TAGCATCTGC CTGATTCTGT TACGGGGTTG GTGATTGACC ATAGGAAGTA TGCAATGTGA     2700

ATCACTGTGT ACAGAGCCGT CTACAACACA TGCTTGACGT TGTAGAGACT GGGACACATA     2760

GCTACCAAGC GGATTAAGTG AAACCTAGAA GGTGTTCAGT ACGTGTGTTG TGTTTCCAAA     2820
```

37

```
ATTCACTGTA CATGATCAGT TTGGTGTTCT TGTACCACAG TTTTTAACCG AAGGAACCAG        2880

TTGGAACAAT CTCAATTTAA CTAAAACTTG AAGAACTAAA ATAACAATGC AAACCTTTAT        2940

CATTGTTTTG GCCAAACTTG TTAAAACTGT AATGCAAGAA CCAAATGCAC TGTGATGTGG        3000

CACCAACTAA TTATGCAAGC ATGAATTTTT CACCTGAGAG TGAAAAAGA AAACTCTACC         3060

ATGGCTTGAA GTTACAGGAG CAGAACTCCT GACTACCATT CTATGACTGA TGAAGAGACT        3120

AATATCTAAA ACCTCAGCAG GCCTTGTTCA CGATATGCAG AAAAAGTGCT GCAGTTTAGA        3180

TACCTCTGGG AACTTTTCCA CAGTGTCACA GGTTTGTAAT ACTTGAAGCC CTTCATTTCT        3240

AAGAATATAT TTCTCGCTCA GTTGTTTCAG GCAAGCCCAA GACTTTGTAA TTTTTAAAGG        3300

GCCCAAGATT TTTTTTTCAA TAACAGACCA GCTTCTTTTT CCTGCAGTTA CAAATGTAAT        3360

TTCTTTTTTT TTTTGTTGTC AAACATAAGG TACCAAATAT GCAATAAATT GTTTTGGG         3418
```

(2) INFORMATION FOR SEQ ID NO: 3:

      (i)   SEQUENCE CHARACTERISTICS
               (A) LENGTH: 1413 base pairs
               (B) TYPE: cDNA
               (C) STRANDEDNESS: both
               (D) TOPOLOGY: Linear

      (ii)   MOLECULE TYPE: cDNA
      (iii)   HYPOTHETICAL: No
      (iv)   ANTISENSE: Yes

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
TCTGGGCTTT CTTTTGAGCT CTTCTTTGTT TATTACGCAG TTTCTTTAGC TCTTTGTCAG          60

ACATGTTTGC TGTATCAGCC TCGTGTTCTT TGTTCTCATC TGTCAGAGGG TTGTCATGAA         120

GCTTCAAATA GATCTCAATA GCAATTCTCG CTGCTTTGAA GTAAAATGGA TGCTGTCGAA         180

GTACATCTTC TAGTTTTAAT AAGTCCACAT ATGATCTAAG GGTGATCTTC CTCATACAGT         240

ATGTATGAAA GTCAAACTGG TCATCGGTGA TTTCTATAAA ATGTCTCTCA ATTTCATGAC         300

ATTTCTTAAG TGCTTCACCA AATTTGTTCA TTGCTTTGTA TGCCTGAGCA CACTCTGTCT         360

GGAACCACAT ACACTGCATT TCATTCAGGT TCTCTACCGC TGAAGTTCCT TCCCTCGTAA         420

ACTTGGAACA CATTTCTTCA GCCTCTTTAA TCAGGTTGGC TTTTAACATG TATTTTGCAC         480

ACTTGGAATT AATAAATCTG TCTGCTGTGT CCAGGGCCTG GGCTTCATCC ATCCACCTGG         540

CAGCTTCTTT AATATTCCCA GCATGCTTAT AGATTTTAGC TTTTACAAGA AAGAGTTCTA         600

TCAATGTTGG TGTACTTTCA ATTGCAGTAT TTATGTATTC CAGAGCAATG GATGGCTGAC         660

CAATTTTATC ATAATGCTGT GCCAAATAGT ACTGGACCCA AAGTAATGTG GTTGGAGGTT         720
```

38

```
CCTCCTTTCC ATCATCATTG GGGTTAAATA GGCGACAACT TTTTAGAGAA GTTTCATAAC      780

CAACTACTAG TTCTTCTACG ATTGCCACCT TCTCTTTATC TCTGTATAAA GACCTCAAGG      840

TATTGAAGAC AGGTGGACAG CCCTTGCTGA AATTCATCCT TAGGAACCTA TCCAAACACT      900

CCTTAAACTT CTCTCCAGAT AAAAAGTTTA AGGGCAGCTT TCTTGGCACG AGTCCCCTGG      960

GGTATTTAGT CCAGGCTTCC TCATATATTT TTAGCCGTTC TAACATATTA GCTGGCTTCA     1020

GTGCTTTTTC TAAGCCTTTG TAATAGGCCC AATTTTCAGG ATTCCTCTCT TGTAATCCTC     1080

TATAAACGTC AGCAGCATCT TCCAAACGAC ACAACTGCAA CAGAAGTTCC CCTTTGGTTT     1140

CTTCAACAGC AAGTTTATCA CAAATCTGCT TTTCATAGGT ACAAAGATGT TCCAGGGCTT     1200

CTCTATAAAG ACCTGCTTCC CGAAGAACTT GATTCTGATA TAAGAGGAGT TCACTATATT     1260

CATAATCCAC TTTATCAGGA GATGTCTGCT GTGTTTTCCT AAACTCTTCT AAAATTTTTG     1320

CTGCCATTTC ATAGTCTTCT AATAAATGGT AAAGCATAAC CAATCCATGA TGCTCACTCT     1380

GCAGATCCTC TATCATCTTG CGGGTGTTAC TTG                                  1413
```

(2) INFORMATION FOR SEQ ID NO: 4:

        (i)   SEQUENCE CHARACTERISTICS
                (A) LENGTH: 3418 base pairs
                (B) TYPE: cDNA
                (C) STRANDEDNESS: both
                (D) TOPOLOGY: Linear

        (ii)   MOLECULE TYPE: cDNA
        (iii)   HYPOTHETICAL: No
        (iv)   ANTISENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
CCCAAAACAA TTTATTGCAT ATTTGGTACC TTATGTTTGA CAACAAAAAA AAAAAGAAAT       60

TACATTTGTA ACTGCAGGAA AAAGAAGCTG GTCTGTTATT GAAAAAAAAA TCTTGGGCCC      120

TTTAAAAATT ACAAAGTCTT GGGCTTGCCT GAAACAACTG AGCGAGAAAT ATATTCTTAG      180

AAATGAAGGG CTTCAAGTAT TACAAACCTG TGACACTGTG GAAAAGTTCC CAGAGGTATC      240

TAAACTGCAG CACTTTTTCT GCATATCGTG AACAAGGCCT GCTGAGGTTT TAGATATTAG      300

TCTCTTCATC AGTCATAGAA TGGTAGTCAG GAGTTCTGCT CCTGTAACTT CAAGCCATGG      360

TAGAGTTTTC TTTTTTCACT CTCAGGTGAA AAATTCATGC TTGCATAATT AGTTGGTGCC      420

ACATCACAGT GCATTTGGTT CTTGCATTAC AGTTTTAACA AGTTTGGCCA AAACAATGAT      480

AAAGGTTTGC ATTGTTATTT TAGTTCTTCA AGTTTTAGTT AAATTGAGAT TGTTCCAACT      540

GGTTCCTTCG GTTAAAAACT GTGGTACAAG AACACCAAAC TGATCATGTA CAGTGAATTT      600
```

```
TGGAAACACA ACACACGTAC TGAACACCTT CTAGGTTTCA CTTAATCCGC TTGGTAGCTA        660

TGTGTCCCAG TCTCTACAAC GTCAAGCATG TGTTGTAGAC GGCTCTGTAC ACAGTGATTC        720

ACATTGCATA CTTCCTATGG TCAATCACCA ACCCCGTAAC AGAATCAGGC AGATGCTAAA        780

GCCCCAACAA CTCTTTGTGC TCAGTGAAAG AATCCAGTGC TAAAACAGCA TTTATTTATG        840

CTGTCTGAGA TATAGCAAAA TCTCACAAGA CAAATTTAAA GTAATATTTC TGCCACACAC        900

CTGCTATGTT AGCTGTTATA GCCTCCAGAT TTTATATAAA TTAGTTAAAA ACATGGGAAG        960

GGAAGGTAGG AATAGGATAC GGATTTTTTT TTCTTTTAAA CCCCTCAATT TTAGCAGCTT       1020

TTAATTTTTT AAGAAACTGA ACCTATATCC TGTAATGTTA GATATTTTAT ATATAGTTTT       1080

CAGCAGGATA AAAAACGTAA GACTATTTGA AGGCAAGAAC ATTTACTCCT CTCATTCTGT       1140

GTAAGTAAGA GCAATGCAGC AGGTGCGTGA CAAAAATATT ATACACTAGA TATGGTCCAA       1200

AGTCATTCCA TTTGCTTGTT TAATGATGTT CAGATTTCAT TGGCCAGTTC TTCCGTTTCT       1260

GCAGAACTAT CTCCGTTCAC TGTGATCTTC ATATCCTCTT CGTATCCAGG AGGCATGAAA       1320

GCCAAAGCAT AAGGGAAAAG CTTATGACAA CTTGCTCTGT AGGCTTCGGC AGCTTCTTTA       1380

CAGTCTCGTA GGCTACCATC ACACAAGGCT TCCAACACTT CCATGCAAGT CTGAAGGTTT       1440

CTGTTGGTGA GGGATCCATC AAGTGTTGTC GCCAGCTCTA TTGCTCGTTT TTGACTAGAA       1500

GAATCTAAAT AATATACCAT TTTGGCAGCT GATAATCTAT GTGGCAATGA ATCAGAATTC       1560

CTTTTCAGAA AGGTTTCATT AAAATTCTTT GGATTGTTG CTCCAAAAAG ACGATTCATT       1620

TCTTGTTTTA ATACTGTTCT AACTGTTTCG GGTAAGTCTT TACTTTCACA CACAGAATGA       1680

AAGAGTCGAA TCATGCACTC ATGAAGCCAG GGATGACTAG AATCAATAGC AAATGCCCGC       1740

TTTACTGATT GTAGCATCAA AAGAAACTTT TCTTTCCTAA AGTAGATCTC AAAGGCAAAA       1800

AGATGAGTTT CTATCTTGTT CTTCACCAAG TTCTTCAATG GTGTTAAAAA CTTAATAGCT       1860

TCTTCCAATG GAGTTTCAAC CTTGGCCAGT TTCTCAGGGA TAAGCTCTTC TTTGGGGCCT       1920

CCAATTTCTT CGTCATCATC ATCCTTTTTC TTTTTCGGAT TCCGTTGCGG CTTTTCTTTT       1980

TCGGCATTTT TTTTCTCTTC TTCAATCTGG GCTTTCTTTT GAGCTCTTCT TTGTTTATTA       2040

CGCAGTTTCT TTAGCTCTTT GTCAGACATG TTTGCTGTAT CAGCCTCGTG TTCTTTGTTC       2100

TCATCTGTCA GAGGGTTGTC ATGAAGCTTC AAATAGATCT CAATAGCAAT TCTCGCTGCT       2160

TTGAAGTAAA ATGGATGCTG TCGAAGTACA TCTTCTAGTT TTAATAAGTC CACATATGAT       2220

CTAAGGGTGA TCTTCCTCAT ACAGTATGTA TGAAAGTCAA ACTGGTCATC GGTGATTTCT       2280

ATAAAATGTC TCTCAATTTC ATGACATTTC TTAAGTGCTT CACCAAATTT GTTCATTGCT       2340

TTGTATGCCT GAGCACACTC TGTCTGGAAC CACATACACT GCATTTCATT CAGGTTCTCT       2400

ACCGCTGAAG TTCCTTCCCT CGTAAACTTG GAACACATTT CTTCAGCCTC TTTAATCAGG       2460

TTGGCTTTTA ACATGTATTT TGCACACTTG GAATTAATAA ATCTGTCTGC TGTGTCCAGG       2520

GCCTGGGCTT CATCCATCCA CCTGGCAGCT TCTTTAATAT TCCCAGCATG CTTATAGATT       2580
```

40

```
TTAGCTTTTA CAAGAAAGAG TTCTATCAAT GTTGGTGTAC TTTCAATTGC AGTATTTATG        2640

TATTCCAGAG CAATGGATGG CTGACCAATT TTATCATAAT GCTGTGCCAA ATAGTACTGG        2700

ACCCAAAGTA ATGTGGTTGG AGGTTCCTCC TTTCCATCAT CATTGGGGTT AAATAGGCGA        2760

CAACTTTTTA GAGAAGTTTC ATAACCAACT ACTAGTTCTT CTACGATTGC CACCTTCTCT        2820

TTATCTCTGT ATAAAGACCT CAAGGTATTG AAGACAGGTG GACAGCCCTT GCTGAAATTC        2880

ATCCTTAGGA ACCTATCCAA ACACTCCTTA AACTTCTCTC CAGATAAAAA GTTTAAGGGC        2940

AGCTTTCTTG GCACGAGTCC CCTGGGGTAT TTAGTCCAGG CTTCCTCATA TATTTTTAGC        3000

CGTTCTAACA TATTAGCTGG CTTCAGTGCT TTTTCTAAGC CTTTGTAATA GGCCCAATTT        3060

TCAGGATTCC TCTCTTGTAA TCCTCTATAA ACGTCAGCAG CATCTTCCAA ACGACACAAC        3120

TGCAACAGAA GTTCCCCTTT GGTTTCTTCA ACAGCAAGTT TATCACAAAT CTGCTTTTCA        3180

TAGGTACAAA GATGTTCCAG GGCTTCTCTA TAAAGACCTG CTTCCCGAAG AACTTGATTC        3240

TGATATAAGA GGAGTTCACT ATATTCATAA TCCACTTTAT CAGGAGATGT CTGCTGTGTT        3300

TTCCTAAACT CTTCTAAAAT TTTTGCTGCC ATTTCATAGT CTTCTAATAA ATGGTAAAGC        3360

ATAACCAATC CATGATGCTC ACTCTGCAGA TCCTCTATCA TCTTGCGGGT GTTACTTG          3418
```

41